

Unexpected findings on the taxonomic status of East Mediterranean *Crocidura russula* auct. (Mammalia, Insectivora)

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Abstract

With an approach, based on chromosomal, biochemical and morphological analyses, we show that the animals which are classically attributed to *C. r. gueldenstaedti* and/or to *C. r. monacha* belong in fact to the taxon *C. suaveolens*. The oriental forms, formerly seen as *C. russula*, are of the same karyotype as *C. suaveolens* and are biochemically close to *C. suaveolens* in Central Europe. The origin of the taxonomical confusion might stem from the large morphological variation in and between populations of *C. suaveolens* in the Near East.

Based on our results *C. russula monacha* Thomas, 1906 belongs to the polymorphic species *C. suaveolens* Pallas, 1811 and we propose to consider *C. (russula) gueldenstaedti* Pallas, 1811 as "incertae sedis".

Introduction

The survey of the literature dealing with the faunistics of the white-toothed shrews *Crocidura* in Europe and in the Near-East reveals that the mainland-inhabiting populations of shrews attributed to *C. russula* present a discontinuous-type distribution.

In fact, two geographical groups of populations are known. On the one hand, populations are abundant and well distributed from the Iberian Peninsula to Central Europe. The eastern border of this area is approximately situated along a line joining the cities of Groningen–Bremen–Dresden–Munich–Vaduz–Martigny–Nice (GENOUD and HUTTERER in prep.; after the original papers of VON LEHMANN 1954; RICHTER 1963; KOCK 1974; ANONYMOUS 1978; HUTTERER 1981). These populations are referred to *C. russula* HERMANN 1780, type locality near Strasbourg, France.

On the other hand, *C. russula* has been recorded in the Near-East region and in the East Mediterranean in the following countries, and under three different names:

- *C. russula* in Turkey (OSBORN 1965; SIMSEK 1980), Lebanon and Israel (JENKINS 1976);
- *C. r. gueldenstaedti* in Turkey (VON LEHMANN 1965; SPITZENBERGER 1970; KUMER-LOEVE 1975)
- *C. r. monacha* in Turkey (JENKINS 1976; ATALLAH 1977), Syria (ATALLAH 1977), Lebanon (HARRISON 1964; ATALLAH 1977) and Israel (HARRISON 1963; HELLWING 1971; ATALLAH 1977).

Moreover, in the Balkans' vicinity, very few animals have been recognized – after morphological examination only – as *C. russula*, among numerous white-toothed shrews of the species *C. suaveolens* and *C. leucodon* in Bulgaria (MARKOW 1957) and in Rumania (MURARIU and ANDREESCU 1982). More recently, samples of *Crocidura* caught in Southern Bulgaria have been analysed biochemically by CATALAN (1984) and morphologically by POITEVIN (1984); only two species were found: *C. leucodon* and *C. suaveolens*, syntopic in three out of six localities.

In addition, shrews of Crete und Cyprus, two Eastern Mediterranean islands, are also referred to *C. cf. russula*: *C. r. gueldenstaedti* on the former (CORBET 1978) and *C. r. cypria* on the latter (ELLERMAN and MORRISON-SCOTT 1966; CORBET 1978).

One should emphasize the lack of data concerning *C. russula* in Thrace (SPITZENBERGER 1970), Greece (ONDRIAS 1965, 1970), Yugoslavia (DULIC and TORTIC 1960) and in the whole of Austria (with the exception of an extreme Western locality: HERZIG and SPITZENBERGER 1977). Finally, the presence of *C. russula* has never been confirmed neither in the southern versant of the Alps nor in the Italian peninsula (MEYLAN and HAUSSER 1974; VON LEHMANN and HUTTERER 1981).

It should be pointed out that *C. russula* sensu stricto and *C. r. gueldenstaedti* – *C. r. monacha* are *allopatric*, and separated by a broad zone without any *russula*-like *Crocidura* as already mentioned by FELTEN et al. (1973).

This discontinuous distribution of *C. russula* is admitted by numerous authors, except RICHTER (1970) who puts forward a daring hypothesis concerning the taxonomy of the forms related to *C. russula*. For RICHTER, *C. russula* HERMANN, 1780 is in fact a super-species, which includes three groups of subspecies: the subspecific group *C. r. russula*, whose geographic repartition is approximately the same as that presented above for the Western European populations of *C. russula*; the subspecific group *C. r. gueldenstaedti* which is a collection of populations inhabiting Turkey, the Near-East countries and the islands of Crete, Cyprus and Corsica; and finally, the third group would be *C. r. suaveolens*, whose very broad repartition comprises the Balkans countries, Thrace and its vicinity, the peninsular Italy and Central Europe up to and including the Iberian Peninsula.

RICHTER's hypothesis has been criticized by several authors who have invoked the following arguments:

- in Western Europe, "there is usually no difficulty in distinguishing *suaveolens* from the subspecies that RICHTER places in the *russula* subspecific group, so *C. suaveolens* should be treated as a separate species" (JENKINS 1976); moreover, *C. russula* and *C. suaveolens* are *sympatric* in countries like France and Spain and their chromosomal complements are quite different (MEYLAN and HAUSSER 1974; SLIVKA 1977);
- by means of the electrophoresis of homologous proteins, the genetic distances calculated between several central European samples of the species *C. russula*, *C. suaveolens* and *C. leucodon*, have shown values as high as those observed between morphologically and cytologically well differentiated species; these results exclude the hypothesis of an intra-specific cluster *C. russula* – *C. suaveolens* versus *C. leucodon* (CATZEFLIS, 1983a).

Nevertheless, a doubt remains about the forms *C. r. gueldenstaedti* and/or *C. r. monacha* since many authors point out the existence of two sympatric forms in the East Mediterranean, besides the bicolored *Crocidura* of the group *C. leucodon-lasia*: (i) a small white-toothed shrew exactly alike the *C. suaveolens* of Western Europe and (ii) a larger shrew very similar to the *C. russula* of Western Europe (SPITZENBERGER 1970; FELTEN et al. 1973; JENKINS 1976; ATALLAH 1977; SIMSEK 1980). Let us recall here that two names have been proposed for the second morphotype: *C. r. gueldenstaedti*, a name derived from *C. gueldenstaedti* Pallas, 1811, whose specific status has been supported by VINOGRADOV (1958), GUREEV (1971) and KOCK (1974), and *C. r. monacha*, described from the North-East of Turkey by THOMAS in 1906.

Analytical methods additional to comparative morphology are necessary to tackle the problematics of taxonomy, e.g. of the forms referred to *C. russula*. For example, CATALAN and POITEVIN (1981) were able to clarify the systematic position of the *Crocidura* of Corsica by using a biochemical method. Consequently, we have combined cytotaxonomical and biochemical approaches, allied with a series of hybridization experiments, whilst adding to our data some morphological considerations.

In this paper, we try to demonstrate that *C. r. gueldenstaedti*, *C. r. monacha* (and probably *C. lasia-lasiura* of Lesbos) are in fact taxonomic units belonging to the species *C.*

suaveolens. Actually *C. suaveolens* is a polymorphic taxon by its morphological and biochemical characters, but has an unchanging karyotype throughout its European and East Mediterranean repartition.

Material and methods

Origin of the animals

Most of the animals analysed here have been caught alive with Longworth traps (Longworth, Abingdon, U. K.). The shrews of Israel come from the Rami Lewi shrew breeding colony kept at the Research Zoo of the Tel-Aviv University, whose founder animals have been caught in the vicinity of Tel-Aviv (HELLWING 1971, 1973).

The white-toothed shrews listed in table 1 can be divided into two sets: on the one hand, several reference samples of the species *C. russula*, *C. suaveolens* and *C. leucodon* originating from Western Europe. The systematics of these three taxonomic units is evident and well accepted by all, as far as Western Europe is concerned. On the other hand, a set of samples from the East Mediterranean region, the taxonomy of which is debated. The populations of this second group have been discreetly

Table 1

Geographic origin and sample sizes of the *Crocidura* populations

Type of analysis: M = morphological; B = biochemical; C = chromosomal

		Number of animals	Analysis
Reference populations			
<i>C. russula</i>			
Cru-1	Morges, Switzerland	26	MBC
Cru-2	Roscoff, France	8	BC
Cru-3	Unhais da Serra, Portugal	12	MBC
Cru-4	Azrou and Oukaimeden, Morocco	7	MBC
<i>C. suaveolens</i>			
Csu-1	Fivizzano, Italy	7	MBC
Csu-2	Mendrisio, Switzerland	7	MBC
Csu-3	Koper (Potok), Yugoslavia	3	BC
Csu-4	Izsak (Fülophasa), Hungary	3	BC
Csu-5	Thessaloniki, Greece	5	MBC
<i>C. leucodon</i>			
Cle-1	Chalais (Réchy), Switzerland	5	MBC
Cle-2	Serramazzone, Italy	6	MBC
Cle-3	Bratislava, Czechoslovakia	3	B
Populations previously referred to <i>C. r. gueldenstaedti</i> , <i>C. r. monacha</i> and <i>C. (r.) cypria</i>			
Csu-6	Izmir, Turkey	7	M C
Csu-7	Kavak (Cakalli), Turkey	7	M C
Csu-8	Maçka (Scalita), Turkey	11	M C
Csu-9	Rize, Turkey	11	M C
Csu-10	Tel-Aviv, Israel	6	MBC
Csu-11	Laxla, Cyprus	5	BC
Csu-12	Troodhos (Prodhromos), Cyprus	13	MBC
Csu-13	Samos: Pagondhas (Ormos Marathokampou) and Neon Karlovasi, Greece	11	M C
Csu-14	Lesbos: Mytilini (Panagiouda) and Ayiasos (Achiaderi), Greece	18	M C
Turkish populations of the <i>C. leucodon-lasia</i> group			
Cle-4	Maçka (Scalita), Turkey	7	M C
Cle-5	Rize, Turkey	11	M C

chosen according to the literature's data and concern some doubtful taxa. Thus, the animals of Cyprus represent the so-called *C. r. cypria* (BATE 1903; CORBET 1978) or *C. cypria* (SPITZENBERGER 1978) or still *C. r. gueldenstaedti* (RICHTER 1970); white-toothed shrews of Samos island are known by the name *C. (r.) gueldenstaedti* (RICHTER 1966); the animals of Scalita (North East Turkey) have been caught in the type locality of *C. r. monacha* THOMAS, 1906 and the other Turkish samples represent what have been called *C. r. gueldenstaedti* (SPITZENBERGER 1970; KUMERLOEVE 1975) or *C. r. monacha* (JENKINS 1976; ATALLAH 1977); finally, the shrews of Tel-Aviv's breeding colony are known under the name *C. r. monacha* (HELLWING 1971, 1973; ZAFRIRI and HELLWING 1973).

The geographic origin of our samples is described in table 1; all the localities can be found in the Time Atlas of the World (1968).

Chromosomal preparations

After the capture, the chromosomal preparation has been carried out in the field for most animals, following the squash method (MEYLAN 1967) or a modified spreading-procedure (after BAKER et al. 1982). In Turkey, we had the possibility to examine at once the prepared karyotypes with a Wild M 11 microscope (Heerbrugg, Switzerland). This allowed us to compare immediately the different

chromosomal sets with the encountered morphological types. Chromosomal preparations were stained with 4% Giemsa (Merck). A minimum number of ten metaphases per individual were analysed on a Wild M 20 microscope. The best kinesis have been photographed at a magnification of 200× to 400×. The diploid number of chromosomes (2N) and the Fundamental Number of arms (NF, including the sex chromosomes) were counted. Finally, the length of each chromosome arm has been expressed as the percentage of the whole length of the female diploid stock, and this for a least two different metaphases per animal (details of the procedure are to be found in MEYLAN and HAUSSER 1973 and HAUSSER 1976).

Morphometry

We carefully took the body and skull measurements in order to obtain reproducible data; with the exception of Cle-3, all the animals were weighted and measured (head and body length HB, tail length TL, hindfoot length HF) shortly after death, and in most cases by the same person.

The skull measurements (fig. 1) have been taken in the laboratory with a Nikon Measuroscope, and all the skulls and jaws have been brought into the same alignment thanks to a set of mirrors (description in HAUSSER and JAMMOT 1974). The measurements CBL (condylobasal length), ZB (maxillary width), OZL (length of upper toothrow) and SKB (braincase breadth) have

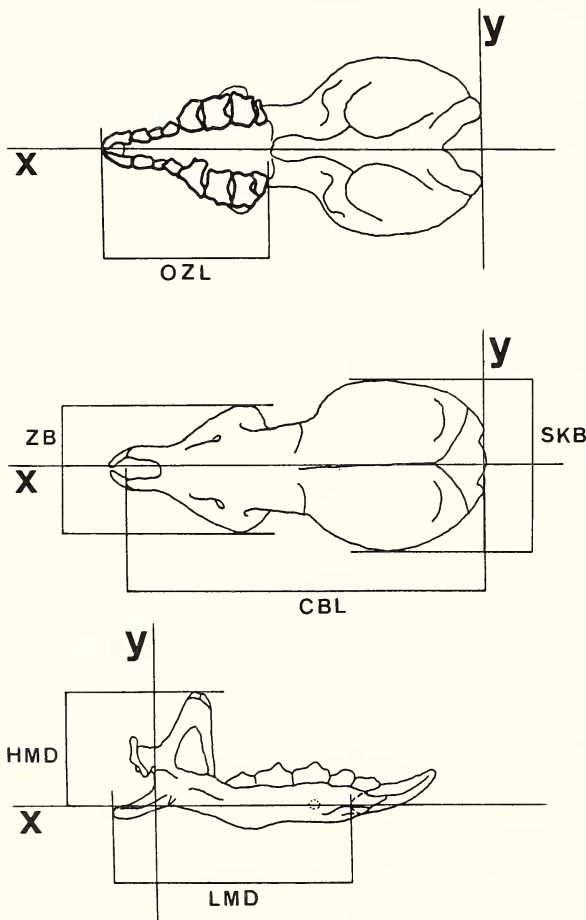


Fig. 1. Skull measurements: the skull and the mandible are positioned according to the XY axes. CBL = condylobasal length; ZB = maxillary width; OZL = upper toothrow length; SKB = braincase breadth; HMD = height of mandible at coronoid process; LMD = length of mandible

been taken according to VESMANIS (1976). The characters HMD (height of mandible at coronoid process) and LMD (length of mandible, excluding incisor) have been examined after alignment of the left mandible as presented in fig. 1.

Electrophoresis

Biochemical analysis has been done through the electrophoresis of homologous proteins encoded by 28 genetic loci, following the general methodology described by BREWER (1970) and SELANDER et al. (1971). The technical data (buffers, staining procedures) concerning our electrophoretic experiments are given in CATZEFLIS (1983a, b) and CATZEFLIS et al. (1982). The standard genetic distances presented here have been computed after NEI's formula (1978) and are based on the between-populations comparisons of the allelic frequencies at the 28 loci listed in table 2.

Hybridization experiments

Hybridization experiments were conducted between shrews of the karyotype $2N = 40$, $NF = 50$ originating from three widely separated localities (Mendrisio, Lesbos and Tel-Aviv). The animals kept in captivity were marked individually and arranged by pairs in small cages (breeding conditions as described by GENOUD and VOGEL 1981).

Conservation of the specimens

All the specimens studied here have been preserved as skulls and skins, or as carcasses in alcohol and skulls, in the collection of the Institute of Zoology and Animal Ecology of the University of Lausanne; karyotypes fixed on slides and histological tissues (liver, kidney, heart) kept in a deep-freezer are deposited in this institution.

Table 2

List of the proteins encoded by the 28 loci, of which the biochemical variations have been surveyed by starch gel electrophoresis. The name of each enzymatic system is preceded by its EC number (Enzyme Classification: International Union of Biochemistry, 1979)

3.1.3.2.	Acid phosphatase: 1 locus
	Albumin: 1 locus
1.1.1.1.	Alcohol dehydrogenase: 1 locus
2.6.1.1.	Aspartate aminotransferase: 2 loci
2.7.3.2.	Creatine kinase: 1 locus
3.1.1.1.	Esterases: 2 loci
4.2.1.2.	Fumarase: 1 locus
1.1.1.49.	Glucose-6-phosphate dehydrogenase: 1 locus
1.1.1.8.	α -Glycerophosphate dehydrogenase: 1 locus
	Hemoglobin (considered 1 locus)
	Hexokinase: 1 locus
2.7.1.1.	Hexose-6-phosphate dehydrogenase: 1 locus
1.1.1.47.	Indophenol oxydase: 2 loci
1.15.1.1.	Isocitrate dehydrogenase: 1 locus
1.1.1.42.	Lactate dehydrogenase: 2 loci
1.1.1.27.	Leucine aminopeptidase: 1 locus
3.4.11.	Malate dehydrogenase: 2 loci
1.1.1.37.	Malic enzyme: 1 locus
1.1.1.40.	Mannose-6-phosphate isomerase: 1 locus
5.3.1.8.	Phosphoglucumutase: 1 locus
2.7.5.1.	6-Phosphogluconate dehydrogenase: 1 locus
1.1.1.44.	Phosphoglucose isomerase: 1 locus
5.3.1.9.	Plasma protein: 1 locus

Results and discussions

Cytological evidence that *C. r. monacha* and *C. r. gueldenstaedti* are specifically different of *C. russula* Hermann, 1780

The main morphological measurements and the observed karyotypes of our samples, compared to a few well known standard populations, are presented in table 3.

A survey of this table puts forward the presence of only three karyotypes, corresponding to what has been described for *C. russula* (SCHMID 1968; MEYLAN and HAUSSEY 1974), *C. leucodon* (MEYLAN 1966; SLIVKA 1977) and *C. suaveolens* (MEYLAN and HAUSSEY 1974; RIMSA et al. 1978). For the bicolored white-toothed shrews of the group *C. leucodon-lasia* we observed in Turkey two very similar karyotypes, both with 28 chromosomes but with Fundamental Numbers 54 and 56 (CATZEFLIS, in prep.).

Table 3

Morphological (mean and standard-error) and chromosomal (2N and NF) characteristics of the reference populations and of the samples referred to *C. r. gueldenstaedti*, *C. r. monacha* and *C. (r.) cypria*

HB = head and body length; TL = tail length; HF = hindfoot length; CBL = condylobasal length; SKB = braincase breadth

Locality	HB	TL	TL/HB	HF	CBL	SKB	Karyotype	Species	
Cru-1 Morges	77.2 ± 4.3	41.7 ± 3.0	54.0 %	12.2 ± 0.5	19.46 ± 0.47	9.42 ± 0.26	2N = 42, NF = 60	<i>C. russula</i>	
Cru-3 Unhais	73.8 ± 2.8	41.2 ± 2.6	55.8 %	11.6 ± 0.3	18.47 ± 0.39	9.03 ± 0.27	2N = 42, NF = 60	<i>C. russula</i>	
Cru-4 Morocco	72.3 ± 5.8	39.8 ± 3.1	55.0 %	12.1 ± 0.9	18.63 ± 0.61	8.80 ± 0.23	2N = 42, NF = 60	<i>C. russula</i>	
Csu-1 Fivizzano	65.6 ± 3.8	41.3 ± 1.7	62.9 %	10.9 ± 0.3	17.05 ± 0.32	8.20 ± 0.17	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-2 Mendrisio	68.4 ± 1.7	36.5 ± 2.6	53.3 %	11.0 ± 0.3	16.75 ± 0.24	8.13 ± 0.17	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-5 Thessaloniki	67.2 ± 6.2	37.6 ± 1.5	55.9 %	11.4 ± 0.4	17.09 ± 0.20	8.26 ± 0.07	2N = 40, NF = 50	<i>C. suaveolens</i>	
Cle-1 Chalais	75.5 ± 7.1	32.6 ± 2.6	43.2 %	11.9 ± 0.6	19.44 ± 0.30	9.27 ± 0.22	2N = 28, NF = 56	<i>C. leucodon</i>	
Cle-2 Serramazzoni	78.3 ± 2.0	39.3 ± 2.9	50.1 %	11.8 ± 0.2	19.21 ± 0.41	9.10 ± 0.19	2N = 28, NF = 56	<i>C. leucodon</i>	
				Other populations					Interpretation
Csu-6 Izmir	75.6 ± 1.8	45.2 ± 1.7	59.8 %	12.5 ± 0.4	18.03 ± 0.31	8.53 ± 0.12	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-7 Cakalli	77.2 ± 2.6	48.4 ± 1.7	62.7 %	13.0 ± 0.4	18.63 ± 0.28	8.92 ± 0.18	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-8 Scaltia	75.4 ± 5.7	47.3 ± 4.0	62.7 %	13.0 ± 0.8	18.23 ± 0.80	8.80 ± 0.31	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-9 Rize	76.3 ± 4.1	51.3 ± 1.8	67.3 %	13.2 ± 0.4	18.48 ± 0.49	9.03 ± 0.18	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-10 Tel-Aviv	72.9 ± 3.0	45.5 ± 2.7	62.4 %	11.6 ± 0.6	17.86 ± 0.60	8.60 ± 0.17	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-12 Troodhos	76.4 ± 2.4	47.6 ± 2.8	62.3 %	12.2 ± 0.4	18.40 ± 0.49	8.51 ± 0.21	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-13 Samos	74.5 ± 2.7	44.3 ± 1.5	59.4 %	11.4 ± 0.4	17.88 ± 0.41	8.75 ± 0.20	2N = 40, NF = 50	<i>C. suaveolens</i>	
Csu-14 Lesbos	71.2 ± 4.2	43.8 ± 1.8	61.5 %	11.6 ± 0.5	17.83 ± 0.47	8.54 ± 0.25	2N = 40, NF = 50	<i>C. suaveolens</i>	
Cle-4 Scaltia	85.0 ± 2.9	44.5 ± 1.9	52.3 %	13.5 ± 0.5	19.92 ± 0.97	9.25 ± 0.34	2N = 28, NF = 54-56	} <i>leucodon-lasia</i> group	
Cle-5 Rize	85.6 ± 3.0	45.8 ± 1.3	53.5 %	13.4 ± 0.4	20.01 ± 0.44	9.31 ± 0.17	2N = 28, NF = 54-56		

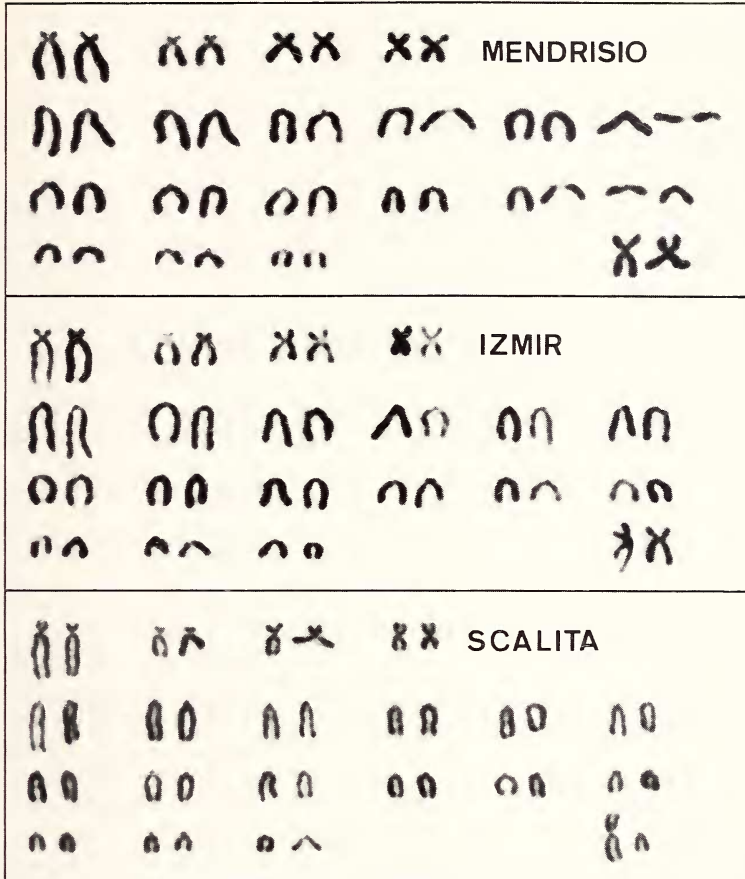


Fig. 2. Karyotypes of some shrews referred here to *C. suaveolens*. Chromosomes are ordered by decreasing length in metacentrics (pairs 1 to 4), acrocentrics (pairs 5 to 19) and heterochromosomes (pair 20). The chromosomal formula is $2N = 40$, $NF = 50$ (female, including the sex chromosomes). Mendrisio: female no. X 859 of Mendrisio, Switzerland; Izmir: female no. X 1297 of Izmir, Turkey; Scalita: male no. X 1321 of Maçka (Scalita), Turkey (type-locality of *C. r. monacha*)

In Turkey, where we have especially looked for as many different types of genus *Crocidura* as possible, only two chromosomal sets were found: the first one is similar with that of *C. suaveolens* and the other agrees with that of *C. leucodon*. As shown in fig. 2 and fig. 3, the white-toothed shrews of Samos, Lesbos and Tel-Aviv have the same karyotype $2N = 40$, $NF = 50$.

Cytological and biochemical evidence that the shrews called *C. r. monacha* and *C. r. gueldenstaedti* are in fact representatives of *C. suaveolens*

In a second step, we arranged the chromosomes of the karyotypes $2N = 40$ and $NF = 50$ in their decreasing length and we compared the relative length of each chromosomal arm, expressed as the percent of the whole length of the female diploid stock. Fig. 4 illustrates the relative lengths (mean and standard-error) of the presumed homologous arms of three *C. suaveolens* from Italy (Fivizzano) and Switzerland (Mendrisio) compared to three individuals from Tel-Aviv and to a pool of ten animals from the Turkish samples of Izmir,

Table 4
Matrix of the standard genetic distances calculated between 15 populations analysed by electrophoresis

	Cru-2	Cru-3	Cru-4	Csu-1	Csu-2	Csu-3	Csu-4	Csu-5	Csu-10	Csu-11	Csu-12	Cle-1	Cle-2	Cle-3
Morges	.051	.058	.025	.531	.548	.520	.523	.632	.492	.545	.544	.475	.483	.478
Roscoff		.059	.039	.477	.491	.467	.475	.576	.514	.522	.535	.544	.514	.544
Unhais da Serra			.010	.508	.525	.497	.504	.599	.537	.469	.505	.551	.499	.546
Azrou				.512	.522	.501	.502	.604	.541	.475	.501	.556	.504	.551
Fivizzano					.079	.004	.105	.131	.171	.152	.141	.456	.391	.441
Mendrisio						.085	.036	.134	.182	.250	.220	.352	.294	.338
Koper							.108	.137	.178	.151	.143	.433	.376	.420
Izsak								.179	.231	.287	.260	.342	.285	.328
Thessaloniki									.124	.193	.182	.424	.349	.418
Tel-Aviv										.113	.097	.285	.277	.287
Laxla/Cyprus											.014	.353	.354	.347
Troodos/Cyprus												.335	.339	.328
Chalais													.078	.001
Serramazzone														.072
Bratislava														

Cakalli, Scalita and Rize. We got a similar alignment of the relative chromosomal lengths for three individuals of Cyprus (CATZEFLIS 1983b), one of Samos and one of Lesbos.

Moreover, a few preliminary results of a comparative G-banding analysis strengthen our opinion that the chromosomal morphology is identical in all the white-toothed shrews with $2N = 40$ and $NF = 50$.

Biochemical results are the most comprehensive to demonstrate that the populations called *C. r. monacha* and *C. r. gueldenstaedti* (at least our geographic samples referring to these two names) are connected to the Western European samples of *C. suaveolens* and do not share any relationships with European populations of *C. russula*. Table 4 presents a matrix of the genetic distances (computed after the allelic frequencies at the 28 surveyed loci¹) between the 15 populations representing the three observed karyotypes.

The matrix of table 4 is illustrated by a dendrogram constructed after the UPGMA procedure (SNEATH and SOKAL 1973) in fig. 5. The cophenetic correlation coefficient between the original data (inputs in the matrix of table 4) and the clustering values (outputs) of the UPGMA dendrogram is 0.971, a high value close to 1, which indicates that the dendrogram is a good interpretation of the matrix' values.

The genetic distances calculated between the populations belonging to the karyotypes characterizing *C. russula* and *C. suaveolens* are very high (mean

¹ The allelic frequencies at the 28 loci characterizing the 15 samples are available upon request at first authors' address.

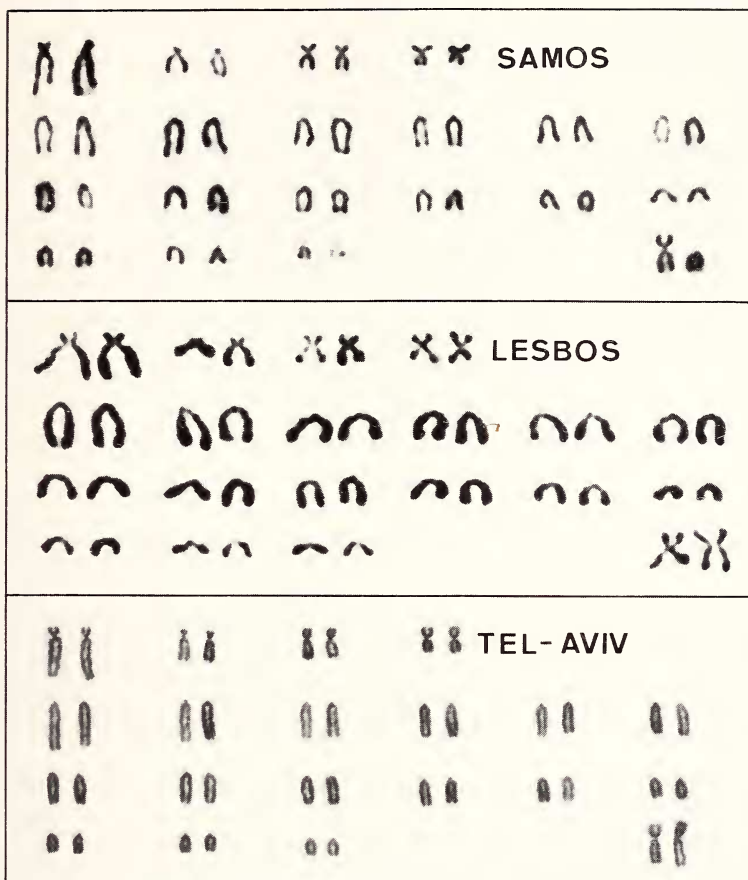


Fig. 3. Karyotypes of some shrews referred here to *C. suaveolens*. Other explanations: see legend of fig. 2. Samos: male no. X 207 of Pagondhas, Samos; Lesbos: female no. X 221 of Mytilini, Lesbos; Tel-Aviv: female no. A 150 of Tel-Aviv, Israel

0.522, range 0.467 to 0.632) compared to the genetic distances computed between population having the same karyotype (table 4). However, we observe a large range in the genetic distances calculated between the samples attributed to *C. suaveolens* (from 0.004 to 0.287), which appears to be a taxon with a high biochemical polymorphism.

Among the populations with $2N = 40$ and $NF = 50$, the samples of Switzerland, Hungary, Italy and Yugoslavia are grouped in a first cluster, then the animals of Thessaloniki fuse with the preceding group. The highest differentiation is observed between the samples of Cyprus and Tel-Aviv versus the European populations; in that comparison, the genetic distances range from 0.124 to 0.287 (mean 0.191).

Hybridization experiments in laboratory: *C. suaveolens* from Mendrisio breeds with $2N = 40$, $NF = 50$ shrews from Lesbos and Tel-Aviv

In our hybridization experiments, a female caught in the island of Lesbos (Csu-14) was successfully crossed with a male from Tel-Aviv (Csu-10), the F1 individuals have bred with animals of the *C. suaveolens* population from Mendrisio (Csu-2), and the hybrids fertility was observed up to the third generation (fig. 6).



Fig. 4. Relative lengths (mean and standard-deviation) of the chromosomal arms in a few shrews referred here to *C. suaveolens*. The chromosomes have been ordered by decreasing length and are presumed homologous. N° chro: number of each chromosomal pair. 1 to 4: long and short arms of the 4 metacentrics x^1 and x^2 : long and short arm of the X-heterochromosome. 1 to 15: relative lengths of the 15 acrocentrics. A: solid line = three individuals from Switzerland (Mendrisio) and Italy (Fivizzano); B: dashed line = ten individuals from Izmir, Cakalli, Maçka and Rize (Turkey)

These experiments demonstrate that there is no genetic incompatibility between these animals having the same chromosomal set but separated by a genetic distance as high (0.182) as the one calculated between Mendrisio and Tel-Aviv samples. This is another argument that shrews sharing the $2N = 40$, $NF = 50$ karyotype in Europe and in the East Mediterranean region belong to the same biological species.

Morphometric data of the $2N = 40$, $NF = 50$ shrews from the type locality of *C. r. monacha* Thomas, 1906

The 11 individuals of population Csu-8 (Scalita: Maçka) originate from the type locality of *C. russula monacha* Thomas, 1906. They have been caught within a radius of 1000 m around the hamlet of Altindere (present name for the ancient Scalita), near the road joining the small city of Maçka to the monastery of Sümela (formerly Meryemanna = Meryam Anna). Table 5 presents the main morphological characteristics of the 11 animals caught from 4th to 9th October 1984 at an altitude of 820 to 880 m. We have added in table 5 the measurements of the holotype and the paratype of *C. r. monacha* (specimens of the British Museum of Natural History) kindly provided by Mrs P. D. JENKINS (in litt.).

On the other hand we have caught in the type locality Scalita (Altindere) 7 *Crociodura* of the group *leucodon-lasia* (karyotype $2N = 28$), and 16 *Sorex raddei*.

Morphological polymorphism in the $2N = 40$, $NF = 50$ populations

The main reason of confusion can probably be explained by the highly variable size of the East Mediterranean populations, which is the expression of an important polymorphism in *C. suaveolens*.

Table 5

Body and skull measurements of the 11 *Crocidura* (having a 2N = 40, NF = 50 karyotype) caught in the type locality of *C. russula monacha* Thomas, 1906 (voucher specimen numbers are those of the collection of the Institute of Zoology and Animal Ecology) and the holotype (***) and paratype (●●●) of *C. r. monacha*

For the abbreviations see fig. 1 and table 1

Number	HB	TL	HF	CBL	ZB	SKB	OZL	HMD	LMD	Sex
X1311	78.0	45.0	13.2	18.76	5.93	8.93	8.37	4.61	9.23	M
X1312	68.0	44.0	12.0	16.70	5.56	8.28	7.90	4.22	8.10	F
X1313	74.0	49.0	13.0	18.57	5.66	8.78	8.44	4.62	9.14	M
X1314	69.5	43.0	12.0	17.34	5.62	8.56	7.77	4.16	8.51	M
X1315	73.0	45.0	13.0	17.88	5.79	8.72	8.26	4.42	8.94	M
X1316	74.0	49.0	13.0	18.32	5.84	8.68	8.42	4.54	9.11	M
X1317	83.0	56.5	13.0	18.86	5.87	8.97	8.37	4.47	9.33	F
X1318	72.0	47.0	13.0	18.30	5.99	8.69	8.47	4.51	9.36	F
X1319	80.5	51.5	14.0	19.27	6.28	9.18	8.67	4.70	9.63	M
X1320	70.5	42.0	12.0	17.28	5.78	8.57	8.05	4.34	8.34	M
X1321	87.0	48.0	15.0	19.24	6.47	9.48	8.38	4.90	9.44	M
***	75.0	44.0	14.0	18.40	5.70	8.60	8.60			F
●●●	70.0	40.0	12.0	17.19	5.68	8.56	7.91	4.07	8.05	F

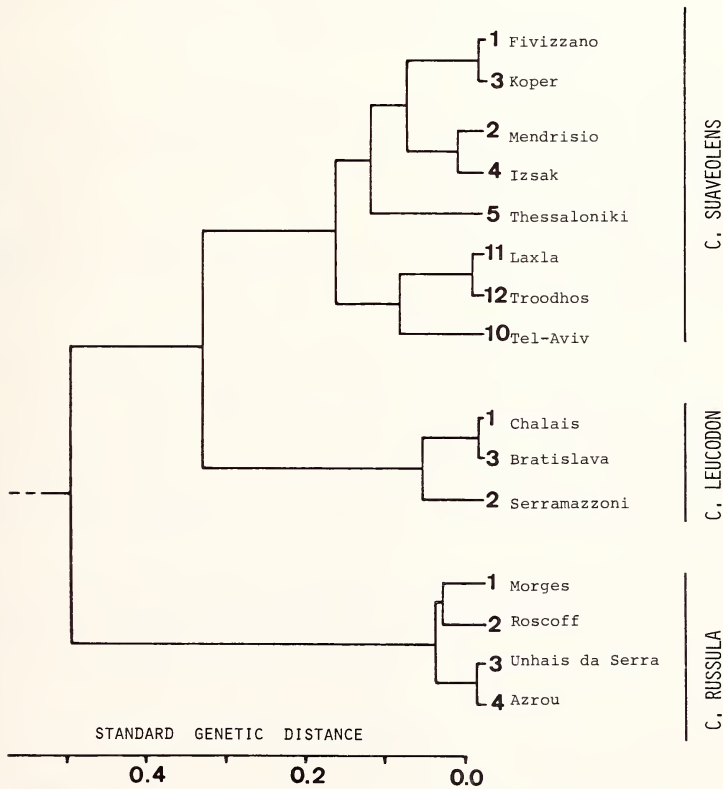


Fig. 5. Dendrogram based on the genetic distances between the populations of the three species of *Crocidura*, constructed according to the UPGMA procedure. The population numbers are the same as in table 1. The cophenetic correlation coefficient is 0.971, a high value which indicates that the dendrogram is a good illustration of the matrix' inputs values

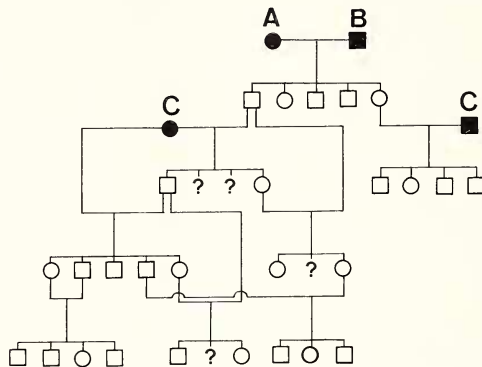


Fig. 6. Hybridization experiments in laboratory between shrews referred to as *C. suaveolens* and originating from different localities. A: female of the island of Lesbos (Csu-14); B: male from Tel-Aviv (Csu-10); C: male and female from Mendrisio (Csu-2); Circle = female; square = male; ? = sex unknown (animals having disappeared after birth)

To sustain this hypothesis, we have examined the range of the most variable body and skull measurements in the 2N = 40, NF = 50 shrews populations. As illustrated in fig. 7, the variation of the condylobasal length CBL shows that the individuals of *C. suaveolens* of Central Europe (for example Mendrisio: 16.75 ± 0.24 mm) are much smaller than those of the Near East (Cakalli: 18.63 ± 0.28 mm). Moreover, one should emphasize that the 2N = 40, NF = 50 sample of the type locality of *C. r. monacha* (CBL: 18.23 ± 0.80) has the same size as the "true" *C. russula* from Portugal (CBL: 18.47 ± 0.39 mm) or from Morocco (CBL: 18.63 ± 0.61 mm).

However, more problematic is to find an explanation why several authors have pointed out the presence of two size-differing sympatric shrews living in Turkey, Lebanon, Syria and Israel, besides the bicolored animals of *C. leucodon-lasia* group (SPITZENBERGER 1970; FELTEN et al. 1973; KUMERLOEVE 1975; ATALLAH 1977; SIMSEK 1980). We suggest here that it is probably the large morphological variability inside the populations of *C. suaveolens* in the East Mediterranean which has induced most authors to consider the larger animals as *C. r. gueldenstaedti* or *C. r. monacha* and the smaller ones as *C. suaveolens*. That amounts to saying that we suspect the separation of one polymorphic species into two artificial taxa according to their size.

To illustrate this possibility, we divided our Turkish 2N = 40, NF = 50 sample (36 animals of the populations Csu-6 to 9) according to the condylobasal length. The 18 smallest animals have a mean CBL of 17.88 ± 0.44 mm and the 18 largest individuals have a mean CBL of 18.81 ± 0.28 mm. The Turkish white-toothed shrews called *C. suaveolens* have a mean CBL of 17.72 mm (28 individuals: FELTEN et al. 1973) or 17.59 ± 0.44 mm (285 animals: SIMSEK 1980), values very similar to our smallest 2N = 40, NF = 50 shrews. The shrews called *C. russula* in Turkey have a mean CBL of 18.68 ± 0.39 mm (275 animals: SIMSEK 1980) and the Turkish *C. r. gueldenstaedti* of FELTEN et al. (1973) have a mean CBL of 18.76 mm (30 individuals), which is the same value as the mean CBL characterizing our 18 largest 2N = 40, NF = 50 animals.

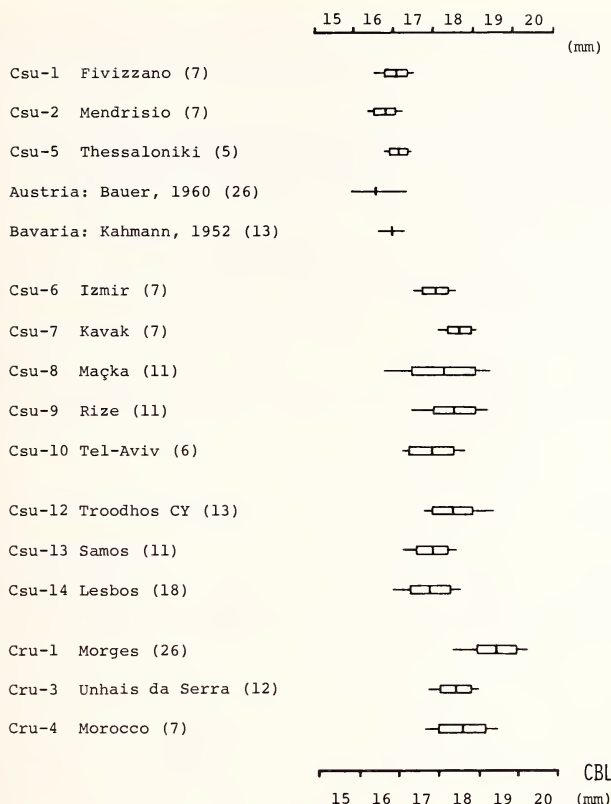


Fig. 7. Variation in the condylobasal length (CBL) by several populations referred to *C. suaveolens* and *C. russula*. Mean, standard deviation and range for each sample measured by us; mean and range for the samples of Bavaria (after KAHMANN 1952) and Austria (after BAUER 1960). The size of each sample is given in brackets.

The problem of *C. gueldenstaedti* Pallas, 1811

Another source of confusion can be attributed to the loss of the holotype and the absence of paratypes of *C. gueldenstaedti* Pallas, 1811. This taxon has been described by Pallas at the same time he named *C. suaveolens*. Let us emphasize that the type localities of both taxa are about 900 km distant, a high value if we accept the idea of a large geographical polymorphism in *C. suaveolens*.

In the lack of type specimens, it is worthless to discuss their taxonomic status. At the least, one could expect to turn *C. gueldenstaedti* into synonymy with another *Crocidurinae* when neotypes originating from Duscheti (Georgia, USSR) will have been analysed morphologically, chromosomally and biochemically.

Conclusions

With the combined adduction of morphological, cytological and biochemical results, we demonstrate that East Mediterranean shrews called *C. russula monacha* and *C. russula gueldenstaedti* do not belong to the Western European taxon *C. russula* Hermann, 1780. It is shown that the Near East *Crocidura* previously reported to as *C. russula* are representa-

tives of the morphologically and biochemically polymorphic species *C. suaveolens* Pallas, 1811. We argue that the form *C. gueldenstaedti* must be considered "incertae sedis" and that the non-bicolored shrews of the type locality of *C. r. monacha* have the chromosomal formula of *C. suaveolens*.

In the present state of our knowledge, one must admit that there are only three species of the genus *Crocidura* living in the mainland parts of Europe and Near East: *C. russula* confined to western Europe, *C. suaveolens* whose large distribution includes the Near East, Caucasus and Balkans' countries and the southern parts of Europe, and finally *C. leucodon* (fig. 8). Concerning the last mentioned species, further analyses are needed to clarify the identity and relationships of the shrews referred to as *C. lasia* and/or *C. lasiura* (according to ONDRIAS 1969) in the Near East.

Finally, it is now possible to discuss the taxonomic status of the Cyprus shrews. Based on the karyotype, CATZEFLIS (1983, b) recognized the close relationship with *C. suaveolens*. However, considering the amount of genetic distance to continental *C. suaveolens* of Europe and the obvious genetic isolation of the island population, he proposed to keep provisionally the name of *C. cypria* Bate, 1903. This prudence was especially indicated as long as the status of the Near Eastern relatives was not cleared up. Taking into account our findings on the large morphological and genetical variations between populations of *C. suaveolens*, it is no longer justified to attribute a specific rank to the Cyprus shrews. To answer the question whether or not a subspecific level – *C. suaveolens cypria* – is justified, samples of populations from Turkey (MADDALENA et al. in prep.) and from Mediterranean islands should be analysed.

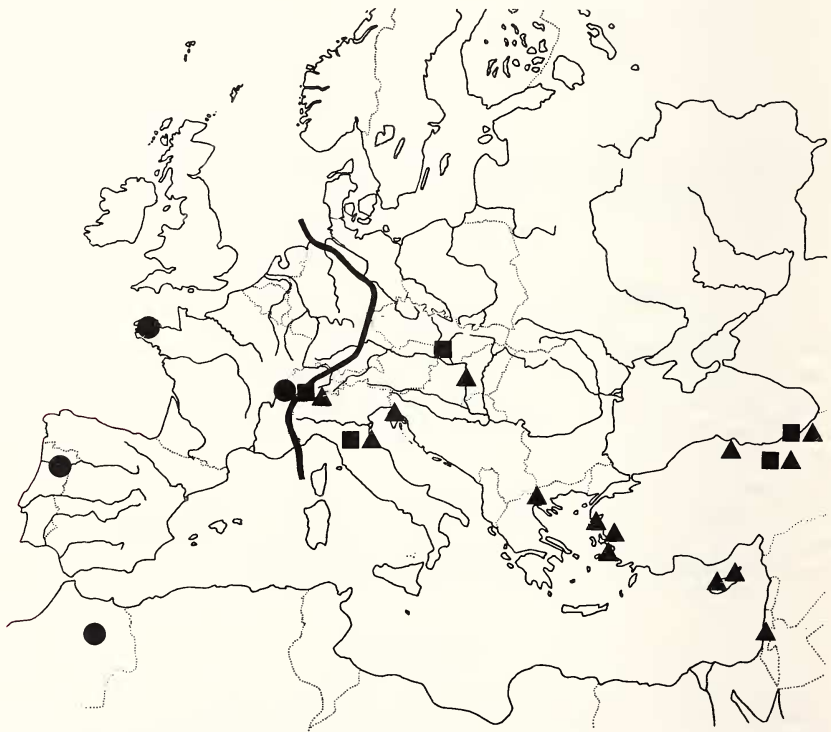


Fig. 8. Geographic origin of the 23 studied samples, according to tables 1 and 3. Circle = *C. russula*; square = *C. leucodon*; triangle = *C. suaveolens*. The dark line marks the eastern border of repartition of *C. russula* Hermann, 1780 in continental Europe. More details in the text

Furthermore, in order to understand evolution and history of *C. suaveolens*, samples of the whole geographic range of this species in Eurasia and Africa should be investigated. This would only be possible with a wide collaboration² of local specialists.

Our results demonstrate that cytology is an adequate method to approach the systematics of the genus *Crocidura* and that hypothesis dealing with the phylogeny of the different Eurasian and African species of this genus must absolutely be based upon the combined informations of several methodologies.

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Résumé

Résultats inattendus sur le statut taxonomique de Crocidura russula auct. (Mammalia, Insectivora) de la Méditerranée orientale

D'après les données de la littérature, la répartition géographique de *Crocidura russula* HERMANN, 1780 serait discontinue et la distribution des animaux rattachés à ce taxon montre deux ensembles de populations. Un premier groupe de populations occidentales se rencontre en Europe de l'Ouest, et est séparé géographiquement d'un second groupe de populations nommées *C. russula monacha* et *C. r. gueldenstaedti* et qui occupent les Pays du Levant et de la Méditerranée Orientale.

Par une approche basée sur des analyses chromosomiques, biochimiques et morphologiques, nous démontrons que les animaux attribués à *C. r. gueldenstaedti* et/ou *C. r. monacha* en Turquie, Chypre et Israël, appartiennent en fait au taxon *C. suaveolens* Pallas, 1811. En effet, les formes orientales attribuées précédemment à «*C. russula*» montrent le même caryotype que *C. suaveolens* et sont biochimiquement proches des échantillons d'Europe centrale de *C. suaveolens*. L'origine de la confusion provient de la grande variabilité morphologique observée entre et à l'intérieur des populations chez les *C. suaveolens* du Proche-Orient.

Sur la base de nos résultats *C. r. monacha* Thomas, 1906 fait partie de l'espèce polymorphique *C. suaveolens* Pallas, 1811 et nous proposons de considérer *C. (russula) gueldenstaedti* Pallas, 1811 comme «incertae sedis».

Zusammenfassung

Unerwartete Ergebnisse zum taxonomischen Status der ostmediterranen Crocidura russula auct. (Mammalia, Insectivora)

Nach Literaturangaben hat *Crocidura russula* HERMANN, 1780 eine diskontinuierliche geographische Verbreitung: Eine erste Gruppe ist im westlichen Nordafrika sowie in West- und Mitteleuropa beheimatet, eine zweite ist im ostmediterranen Raum sowie im Nahen Osten verbreitet. Tiere der östlichen Gruppe werden meistens als *C. russula monacha* oder *C. russula gueldenstaedti* bezeichnet.

Unter Einbeziehung cytologischer, biochemischer und morphologischer Methoden wurden Vertreter der östlichen Gruppe analysiert und mit Tieren der drei mitteleuropäischen *Crocidura*-Arten verglichen. Dabei zeigt sich, daß *C. r. monacha* und/oder *C. r. gueldenstaedti* aus Israel, Türkei und Zypern nicht zu *C. russula* HERMANN, 1780 sondern zu *C. suaveolens* Pallas, 1811 gehören. Sie besitzen alle denselben Karyotyp (2N = 40, NF = 50), sind sich biochemisch sehr ähnlich und lassen sich mit Tieren aus Griechenland (Lesbos) und der Schweiz kreuzen. Die bisherige falsche Zuordnung läßt sich durch die große morphologische Variabilität erklären, welche innerhalb und zwischen nächstöstlichen Populationen von *C. suaveolens* gefunden wird.

Auf Grund der Ergebnisse, insbesondere der Chromosomenbefunde von Tieren der Terra typica, gehört *C. russula monacha* Thomas, 1906 zur polymorphen Art *C. suaveolens* Pallas, 1811. *C. (russula) gueldenstaedti* Pallas, 1811 ist als „incertae sedis“ zu betrachten.

² For collaboration please take contact with P. VOGEL, Lausanne.

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